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re greater than or equal to the score of the result being printed,
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Best Local Similarity
Matches 43; Conserv
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Q9SPL3;
Q1-MAY-2000 (TrEMBLrel. 13, Created)
Q1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
Q1-OCT-2000 (TrEMBLrel. 15, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                Macadamia integrifolia (Macadamia nut).
Macadamia integrifolia (Macadamia nut).
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; Proteaceae; Macadamia.
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SEQUENCE
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Marcus J.P., Goulter K.C., Green J.L., Manners J.M.;
Marcus J.P., Goulter K.C., Green J.L., Manners J.M.;
"A family of antimicrobial peptides is produced by processing of a 7S
"A family of antimicrobial integrifolia.";
globulin protein in Macadamia integrifolia.";
                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=60698;
                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
Q9SPL5;
01-MAY-2000 (TrEMBLrel.
                      Q9SPL5
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                       PRELIMINARY;
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   13,
   Created)
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                                                                                                                              Score 248; DB 10;
Pred. No. 8.3e-22;
; Mismatches 0;
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                            666
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Matches 42
     Q9SEW4;
Q9SEW4;
01-MAY-2000
01-MAY-2000
                                                                                                                                                                    MATCUS J.P., GOULTEY K.C., Green J.L., Manners J.M.;
"A family of antimicrobial peptides is produced by pr
globulin protein in Macadamia integrifolia.";
Plant J. 0: 0-0(1999).
EMBL; AF161884; AAD54245.1; -.
HSSP; P02853; 2PHL.
INTERPRO; IPRO01113; -.
PFAM; PF00546; Seedstore_7s; 1.
SEQUENCE 666 AA; 78243 MW; 0ECA22F8710F8A7B CRC64
                                                                                                                                                                                                                                                                                                                                                     01-MAY-2000
01-MAY-2000
01-OCT-2000
                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
TISSUE=NUT KERNEL;
                                                                                                                                                                                                                                                                                        Macadamia integrifolia (Macadamia nut).
Eukaryota; Viridiplantae; Embryophyta; Trao
Magnoliophyta; eudicotyledons; Proteaceae;
NCBI_TaxID=60698;
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"A family of antimicrobial peptides is produced by processing globulin protein in Macadamia integrifolia kernels.";

Plant J. 0:0-0(1999).
                                                                           Macadamia integrifolia (Macadamia nut).
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; Proteaceae; Macadamia.
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01-OCT-2000 (TrEMBLrel.
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40; Conservative
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NCE 666 AA; 78217 MW;
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P02853; 2PHL.
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    (TrEMBLrel.
                                 PRELIMINARY;
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15,
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                                                                                                                  Score 235; DB 10
Pred. No. 3e-20;
2; Mismatches
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Pred. No. 5.9e-21;
0; Mismatches 1;
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Best Local s
Matches 20
                                                                                          CHAIN
SEQUENCE
                                                                                                                                                    McHenry L., Fritz P.J.;

"Comparison of the structure and nucleotide sequences of vicilin genes of cocoa and cotton raise questions about vicilin evolution.";

Plant Mol. Biol. 18:1173-1176(1992).

EMBL; X62625; CAA44493.1;

EMBL; X6266; CAA44494.1;

HSSP; P02853; 2PHL.

MENDEL; 30919; Theoc;1188;30919.
                                                                                                              SIGNAL
                                                                                                                         Signal.
                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1996
01-NOV-1996
01-OCT-2000
                                                                                                                                 PRODOM; PD081059; -;
                                                                                                                                              INTERPRO; IPRO01113; PFAM; PF00546; Seeds
                                                                                                                                                                                                                                                                                              Theobroma cacao (Cacao).

Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;

Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;

Malvales; Malvaceae; Theobroma.
                                                                                                                                                                                                                                                MEDLINE=92288309; PubMed=1600151;
                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                            NCBI_TaxID=3641;
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Q43358;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.

STRAIN-CV. SUNLAND; TISSUE-SOMATIC EMBRYO LINE;
Teuber S.S., Jarvis K.C., Peterson W.R., Dandekar A.M., Ansari A.A.;
"Identification and cloning of a cDNA encoding a vicilin-like protei
Jug r 2, from English walnut kernel (Juglans regia): a major food
allergen.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-OCT-2000 (TrEMBLrel 15, Last annotation update) VICILIN-LIKE PROTEIN PRECURSOR (FRAGMENT).
Juglans regia (English walnut).
Eukaryota; viridiplantae; Embryophyta; Tracheophyta Magnoliophyta; eudicotyledons; core eudicots; Rosid NCBI_TaxID=51240;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AF066055; AAE
HSSP; P02853; 2PHL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted
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QEDPQTECQQCQRRCRQQESDPRQQQYCQRRCKEICEEEE
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                                              Similarity
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20; Conservative
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525
. 60798 MW;
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47.58;
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01,
                                  10;
                            Score 110; DB 10;
Pred. No. 1.3e-05;
Pred. No. 1.3e-11;
                                                                                                VICILIN
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Last annotation updat
                                                                                                         POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                        Created)
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Pred. No. 8.4e
7; Mismatches
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                                                                                 19114CD5C248905D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
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                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 593;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0
                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                           0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0
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Length

425;

Indels

23;

Gaps

2

ROOQYCORRCKEICE

314 38

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2
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P91419
                                                                                                                                                                                                                                                                                                                                                                                                                                                             B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A LO CONTRACTO CONTRACTOR CONTRAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local S
Matches 17
                                                                                                                                                                                                                                         017400;
01-JAN-1999
01-JAN-1999
01-JAN-1999
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01-MAY-1997
01-NOV-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P91419;
P91419;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A
Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
Jones M., Kershaw J., Kirsten J., Liaister N., Latreille P.,
Jones M., Kershaw J., Kirsten J., Liaister N., Latreille P.,
Lightning J., Lloyd C., Mcmurray A., Mortimore B., O'Callaghan M.,
Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen
Smaldon N., Smith A., Sonnhammer E., Staden R., Sulston J.,
Ballon N., Smith A., Sonnhammer E., Staden R., Sulston J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases EMBL; U80455; AAB37887.1; -. SEQUENCE 411 AA; 44675 MW; 599DAC9DCFAB1382 CRC64;
                           STRAIN-BRISTOL N2;
                                                      SEQUENCE FROM N.A
                                                                                                                        Eukaryota; Metazoa;
Rhabditidae; Pelode
                                                                                                                                                                  Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. STRAIN=BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Watson A., Weinstock L
"2.2 Mb of contiguous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Thierry-Mieg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Caenorhabditis elegans
Eukaryota; Metazoa; Nem
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  T01D1.6
                                                                                                                                                                                                                   HYPOTHETICAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Waterston R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (JAN-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bradshaw H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=BRISTOL N2;
MEDLINE=94150718; PubMed=7906398;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CODED FOR BY
                                                                                               NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nature 368:32-38(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rhabditidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        σ
                                                                                                                                                                                                                                                                                                                                                                                                                                                        QQPAQQQCQQDCQAACPQQQ----QPQQQCQQQCQTTCQSDDQY 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QEDPOTECOO-CORRCROQESDPROQOYCORRCKEICEEEEEY 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EEELQRQYQQCQGRCQEQQQGQREQQQCQRKCWEQYKEQE 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     l Similarity
17; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         eg J., Thomas K., Vaudin M., Vaughan K., Waterston R., Weinstock L., Wilkinson-Sproat J., Wohldman P.; contiguous nucleotide sequence from chromosome III of
                                                                                                                                                                                                                 (TremBLrel. 09, Created)
(TremBLrel. 09, Last sequence update)
(TremBLrel. 09, Last anotation update)
L 45.9 KDA PROTEIN AC3.3 IN CHROMOSOME V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Wohldmann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ი.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Peloderinae;
                                                                                                                           Peloderinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ELEGANS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nematoda;
                                                                                                                                                 Nematoda;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         38.7%;
39.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6
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o the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              03,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          oda; Chromadorea; Rhabditida;
Caenorhabditis.
                                                                                                                           Caenorhabditis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 96; DB
Pred. No. 0.00
11; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Last sequence up
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YK115A6.5.
                                                                                                                                            Chromadorea;
                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                    425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 5;
                                                                                                                                                                                                                                                                                                                                    AΑ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         update)
on update)
                                                                                                                                              Rhabditida;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 411;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                   PRECURSOR
                                                                                                                                              Rhabditoidea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rhabditoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Shownkeen R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           III of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Α
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2
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RESULT
Q19594
ID QI
AC QI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
watches 17; Conserv
                                                                                                                                                                                        Ωy
                                                                                                                                                                                                                                            밁
                                                                                                                                                                                                                                                                                   δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ωy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DЬ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CCC CCC DR DR DR FT FT SQ
                                                                                                                                              Ъ
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                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q17401
Q17401;
Q1-JAN-1999
Q1-JAN-1999
Q1-JQN-2000
  Q19594
Q19594;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AC3.4.
Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea;
Eukaryota; Metazoa; Nematoda; Chromadorea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TRANSMEM
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (PO-!- SIMILARITY: BELONGS TO FAMILY UPF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; Z71177; CAA94868.1; WORMPEP; AC3.4; CE05134. INTERPRO; IPR001594; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hypothetical protein; Signal. SIGNAL 1 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases -:- SIMILARITY: BELONGS TO FAMILY UPF. EMBL; Z71177; CAA94867.1; -. WORNDEP; AC3.3; CE05133.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hypothetical protein; Transmembrane.
TRANSMEM 309 329 POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRODOM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PFAM; PF01529; zf-DHHC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mcmurray A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HYPOTHETICAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=6239;
                                                                                                                                              182 Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   315 Q 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              255
                                                                                                                                                                                                                                         122
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                                                                                                                                                                                           39 E
                                                                                                                                                                                                                                                                                      2 QEDPQTECQQCQRRCR---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 QEDPQTECQQCQRRCR------QQESDP-----
                                                                         9
                                                                                                                                                                                                                                       QQPSAPQCQQCQNTCQQAAPVCQQQCAPQCQQQSAPACQQCQTSCQQTQQCQQQCTPQCQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QQPSAPQCQQCQNTCQQAAPVCQQQCAPQCQQQSAPACQQCQTSCQQTQQCQQQCTPQCQ
                                                                                                                                                                                                                                                                                                                                  ch 31.
l Similarity 27.
17; Conservative
                                                                                                                                              182
                                                                                                                                                                                             39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PD003041;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             425 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (TrEMBLrel. 09, Created)
(TrEMBLrel. 09, Last sequence update)
(TrEMBLrel. 14, Last annotation update)
L 67.7 KDA PROTEIN AC3.4 IN CHROMOSOME V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       490
                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22
                                                                                                                                                                                                                                                                                                                                                                                                                                                        AΑ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      510
287
67740
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               467
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27.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             45922 MW;
                                                                                                                                                                                                                                                                                                                                                             .98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL.

POTENTIAL.

GLN-RICH.

504A5CE1BA72091B (
                                                                                                                                                                                                                                                                                                                                    9;
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                                                                                                                                                                                                                                                                                                                                                      Score 78.5;
Pred. No. 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 78.5;
Pred. No. 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HYPOTHETICAL PROTEIN AC3. 951352A2AFF7E96C CRC64;
                                                                                                                                                                                                                                                                                                                                    Pred. No. 0.0'
); Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POTENTIAL
                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                      -QQESDP---
                           572
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               600
                                                                                                                                                                                                                                                                                                                                                             .074;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .056;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AA
                                                                                                                                                                                                                                                                                                                                                                                   DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DВ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROTEIN (POTENTIAL)
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CRC64;

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ACCOMENS ACCORDANT ACCOR
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017970;
01-JAN-1998 (TrEMBLrel. 0
01-JAN-1998 (TrEMBLrel. 0
01-OCT-2000 (TrEMBLrel. 1
M02G9.1 PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                            Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A
Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
Lightning J., Lloyd C., McGmurray A., Mortimore B., O'Callaghan M.,
Parsons J., Parcy C., Rifken L., Roopra A., Saunders D., Shownkeen
Smaldon N., Smith A., Sonnhammer E., Staden R., Sulston J.,
Batter M., Sulsto
                                                                                                                                                  Nature 368:32-38(1994).
EMBL; Z81573; CAB04625.1; -.
HSSP; O46655; 1CJH.
SEQUENCE 1513 AA; 161578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Caenorhabditis elegans.
Eukaryota; Metazoa; Nemat
Rhabditidae; Peloderinae;
                                                                                                                                                                                                                                                                                    elegans.
                                                                                                                                                                                                                                                                                                                                          Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterst
Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.;
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NCBI_TaxID=6239;
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01-JUN-1998 (TrEMBLrel.
01-OCT-2000 (TrEMBLrel.
HYPOTHETICAL 62.4 KDA PR
                                                                                                                                                                                                                                                                                                          "2.2 Mb of contiguous nucleotide sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. MEDLINE=94150718; PubMed=7906398;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted
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SIGNAL 1 21
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Submitted (APR-1996)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Caenorhabditis elegans
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=6239;
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17; Conser
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17; Conserv
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572 AA;
         Conservative
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BLrel. 06, Last sequence update)
BLrel. 15, Last annotation update)
KDA PROTEIN F19G12.7 IN CHROMOSOME
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                                                                                                                                                           161578 MW;
                                  31.0%;
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Caenorhabditis.
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Score 77; DB Pred. No. 0.24
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Created)
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HYPOTHETICAL PROTEIN F19G12.7.
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                                                                                                                                                           1.0BCB4287BA282E5 CRC64;
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                               DB 5;
0.24;
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      16;
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                                                            Length 1513;
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                                                                                                                                                                                                                                                                                                                chromosome
      Indels
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MUITRY J., Le T.T.;
Submitted (MAY-1996) to the EMBL/GenBi-
-!- SIMILARITY: BELONGS TO FAMILY UPF
EMBL: U58742; AAB36856.1; --
WORMPEP; F31A3.1; CE07158.
Hypothetical protein; Transmembrane.
TRANSMEM
3 23 POTENTIAL
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01-JAN-1998 (TrEN
01-JAN-1998 (TrEN
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C03A7.4 PROTEIN.
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Q19919;
Q1-JUN-1998
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O1-JUN-1998
                                                                                                  Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L., Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L., Johnston R., Kershaw J., Kirsten J., Laister N., Latreille P., Lightning J., Lloyd C., Mcmurray A., Mortimore B., O'Callaghan M., Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen Smaldon N., Smith A., Sonnhammer Ladden R., Sulston J., Thomas K., Vaudin M., Vaughan K., Waterston R., Water
                      Nature
[2]
SEQUENCE FROM N.A
                                                                elegans
                                                                                                                                                                                                                                                                                                                      STRAIN=BRISTOL N2;
MEDLINE=94150718; PubMed=7906398;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Nemat
Rhabditidae; Peloderinae;
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Eukaryota; Metazoa; Nemat
Rhabditidae; Peloderinae;
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Bonfield J., Burton J., Connell M., Copsey T., Cooper J.,
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                                                                              "2.2 Mb of contiguous nucleotide sequence from chromosome
                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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                                          368:32-38(1994)
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(TrEMBLrel. 06, Last annotation update)
26.2 KDA PROTEIN F31A3.1 IN CHROMOSOME
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                                                                                                                                                                                                                                                                                                       Submitted EMBL; AF01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A
Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
Lightning J., Lloyd C., Mcmurray A., Mortimore B., O'Callaghan M.,
Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen I
Smaldon N., Smith A., Sonnhammer E., Staden R., Sulston J.,
This could be supported by Morting R., Sulston J.,
This could be supported by Morting R., Sulston J.,
This could be supported by Morting R.,
This could be supported by 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R., Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.; "2.2 Mb of contiguous nucleotide sequence from chromosome III of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (JUL-1997) to the EMBL/GenBank/DDBJ databases EMBL; AF016451; AAB66001.1; -. SEQUENCE 388 AA; 42139 MW; 2E20655B0B9AE492 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=BRISTOL N2;
Greco T., Bradshaw H.,
Submitted (AUG-1997) t
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MEDLINE=94150718; PubMed=7906398;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa;
Rhabditidae; Pelode
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                                                                                                                                                                                                                                                                              SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nature 368:32-38(1994).
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194
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                                                   QEDPQTEC-QQCQRRCRQQESDPRQ-QQYCQRRCKEICEE 39
                                                                                                                                                                                                                                                                                                       tted (JUL-1997) to the EMBL/GenBank/DDBJ databases AF016451; AAB65996.1; -.
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Caenorhabditis.
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Pred. No. 0.13
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EMBL; AF03
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Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.
Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.
Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
Lightning J., Lloyd C., Memurray A., Mortimore B., O'Callaghan M.,
Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen
Smaldon N., Smith A., Sonnhammer E., Staden R., Sulston J.,
Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.;
"2.2 M of contiguous nucleotide sequence from chromosome III of C
                                  Eukaryota; Metazoa; Nemat
Rhabditidae; Peloderinae;
RNBI_TaxID=6239;
                                                                                                      C03A7.8.
Caenorhabditis elegans
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MEDLINE=94150718; PubMed=7906398;
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Eukaryota; Metazoa; Nemat
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SEQUENCE FROM N.A.
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RA Bonfield J., Burton J., Connell M., Copey T., Cooper J., Cooper J.,
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RA Bonfield J., Burton J., Connell M., Copey R.,
RA Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
RA Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
RA Jones M., Kershaw J., Kitsten J., Laister M., Latreille P.,
RA Lightning J., Lloyd C., Memurray A., Mortimore B., O'Callaghan M.,
RA Jones M., Kershaw J., Kitsten J., Laister M., Latreille P.,
RA Smaldon N., Santh A., Sonnhammer E., Staden R., Sulston J.,
RA Smaldon N., Santh A., Sonnhammer E., Staden R., Sulston J.,
RA Staden R., Walkinson-Sproat J., Wohldman P.,
RA Staden R., Walkinson-Sproat J., Wohldman P.,
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